

ABSTRACT

The present invention provides an integrated system capable of selectively retrieving and concentrating specific biomolecules from biological media for subsequent high-performance analyses, quantifying targeted proteins, recognizing variants of targeted biomolecules (e.g., splice variants, point mutations and post-translational modifications) and elucidating their nature, analyzing for, and identifying, ligands interacting with targeted biomolecules, and high-throughput screening of large populations of samples using a single, unified, economical, multiplexed and parallel processing platform. The preferred embodiment of the integrated system comprises molecular traps, such as affinity microcolumns, derivatized mass spectrometer targets, mass spectrometers capable of multi-sample input and robotics with processing/data analysis interactive database. The present invention also includes methods and processes for use of the individual components and the integrated system in biological applications. Furthermore, the preferred embodiment of the present invention provides for the preparation and/or processing of multiple separate devices and/or samples to accomplish high throughput analysis.